

From: Fredman, Jeffrey
Sent: Monday, August 12, 2002 2:31 PM
To: STIC-Biotech/ChemLib
Cc: Angell, Jon E
Subject: FW: Sequence Database Search Request

PLEASE RUSH.

I APPROVE.

Jeff Fredman
(Eric, I got it the second after I called you)

Point of Contact:
Mona Smith
Technical Information Specialist
CM1 6A01
Tel: 308-3278

-----Original Message-----

From: Angell, Jon E
Sent: Monday, August 12, 2002 2:31 PM
To: Fredman, Jeffrey
Subject: Sequence Database Search Request

SEARCH REQUEST FORM
Scientific and Technical Information Center

Examiner# : 78697
Art Unit : 1635
Phone Number: 605-1165
Date: 8/12/02
Serial Number: 09/786,043
Mailbox & Bldg/Room Location: CM1-11E12
Results Format Preferred (circle): Paper

RECEIVED
AUG 12 2002
STIC

I would like to have a search performed using the following SEQ. ID NOs. from application : 09/786,043

SEQ ID NO. 1-- nucleic acid seq. (<900nucleotides in length)
SEQ ID NO. 2-- amino acid seq. (255 amino acids in length)

NOTE: Please reverse transcribe SEQ ID NO:2 into nucleic acid encoding the seq of SEQ ID NO:2.

I would like a standard search of SEQ ID NO.1 and the cDNA encoding SEQ ID NO:2 , AND an oligomer search of the cDNA encoding SEQ ID NO:2 to identify nucleotide oligos encoding at least 10 contiguous amino acids of SEQ ID NO: 2.

Thanks,
Eric

J. Eric Angell
Art Unit 1635
CM1 12D15
703-605-1165
mailbox CM1 11E12

TYPE OF SEARCH:		VENDOR/COST (where applic.)
Searcher: <u>M. Smith</u>	NA Sequences: <u>1</u>	STN: _____
Phone: _____	AA Sequences: <u>3</u>	DIALOG: _____
Location: _____	Structures: _____	Questel/Orbit: _____
Date Picked Up: <u>8/13/02</u>	Bibliographic: _____	DRLink: _____
Date Completed: <u>8/14/02</u>	Litigation: _____	Lexis/Nexis: _____
Searcher Prep/Review: <u>10</u>	Full text: _____	Sequence Sys.: _____
Clerical: _____	Patent Family: _____	WWW/Internet: _____
Online time: <u>15</u>	Other: _____	Other (specify): _____

DR InterPro: IPR003118; SAM_PNT.
 DR Pfam: PF00178; Ets; 1.
 DR Pfam: PF02198; SAM_PNT; 1.
 DR PRINTS: PRO0454; ETSDOMAIN.
 DR SMART: SM00413; ETS; 1.
 DR SMART: SM00251; SAM_PNT; 1.
 DR PROSITE: PS50061; ETS_DOMAIN; 3; 1.
 DR SEQUENCE 300 AA; 34893 MW; 51CB68E6195AE06 CRC64;

Query Match 40.7%; Score 574; DB 4; Length 300;
 Best Local Similarity 41.3%; Pred. No. 2.6e-47;
 Matches 117; Conservative 47; Mismatches 63; Indels 56; Gaps 8;

QY 22 SMTDLFSNEEYYPAREHOTACDYSYTSVHPREYWKRRHWEMLOFCCDQYKLDINCISFCN 81
 Db 23 AWTDSYPTCNVSSGF-----FGSOWHEIHPOYWKYQVEMLOHLLDINQDASCIPIFOE 77
 QY 82 FNISGLQCSMTQEEFEVNAAGLCEGYLYFIIONIRTOG-----YSPFNDAEESKA 131
 Db 78 FDISGHEHCSMSLOEFTTRAAGAGQLLYSNLOHLKMGCCSSDLFQSTHNYIVKTEQTEP 137
 QY 132 TIKD-VYDSNCL-----KTSGI-----KSD-----C 152
 Db 138 SIMNTWKEENYLYDPSYGVLDLSDKTCFRAQISMTTSHLPVASEPDKKEQDPAPAC 197
 QY 153 HSRTSLSOSHMEFVRDLLSPENCILWEDEBOGIFRYVKSALAKMGQRRKND 212
 Db 198 HT-KKHNPGRGTHMEFRIDLLSPDKNPGLIKWEDSEGFRLKSEAVAOIMGKKNNSS 256
 QY 213 RTVEKLSRALRYKYKTLGERVD-RRLVYKFGKNAHQEDK 254
 Db 257 SMTYELSRAMRYKYKREILERVGRRLVYKFGKNAHQRENE 299

RESULT 12

ID 070273 PRELIMINARY; PRT; 300 AA.
 AC 070273:
 DT 01-AUG-1998 (TREMBLrel. 07, Created) *Accession: AF05507*
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE EHF.
 GN EHF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=PIUTARY;
 RX MEDLINE=98262938; PubMed=9600089;
 ROBERT M. A., Kleinbaum L.A., Sun L.Y., Burton F.H.;
 "Molecular cloning and expression of Ehf, a new member of the ets
 transcription factor/oncogene family.";
 RL Biochem. Biophys. Res. Commun. 246:176-181(1998).
 DR EMBL: AF05527; AAC40119.1; -
 DR HSSP: Q00422; IAWC.
 MGD: MGI:1270840; Ehf.
 DR InterPro: IPR000418; Ets.
 DR InterPro: IPR002341; HSF_ETS.
 DR Pfam: PF00178; SAM_PNT.
 DR Pfam: PF02198; Ets; 1.
 DR PRINTS: PRO0454; ETSDOMAIN.
 DR SMART: SM00413; ETS; 1.
 DR SMART: SM00251; SAM_PNT; 1.
 DR PROSITE: PS50061; ETS_DOMAIN; 3; 1.
 DR SEQUENCE 300 AA; 34903 MW; 91D9477EFB874747 CRC64;

Query Match

Similarity 40.3%; Score 568; DB 11; Length 300;
 42.6%; Pred. No. 9.9e-47;

Matches 120; Conservative 39; Mismatches 69; Indels 54; Gaps 7;

QY 22 SMTDLFSNEEYYPAREHOTACDYSYTSVHPREYWKRRHWEMLOFCCDQYKLDINCISFCN 81
 Db 23 AWTDSYPTCNVSSGF-----FGSOWHEIHPOYWKYQVEMLOHLLDINQDASCIPIFOE 77
 QY 82 FNISGLQCSMTQEEFEVNAAGLCEGYLYFIIONIRTOG-----YSPFNDAEESKA 131
 Db 78 FDISGHEHCSMSLOEFTTRAAGAGQLLYSNLOHLKMGCCSSDLFQSTHNYIVKTEQTEP 137
 QY 121 SPFNDAE-----SKATIKDYADSNCLKTSGI-----KSD-----CHS 154
 Db 138 SIMNTWKEENYLYDPSYGVLDLSDKTCFRAQISMTTSHLPVASEPDKKEQDPAPAC 197
 QY 155 HSRT-SLSOSHMEFVRDLLSPENCILWEDEBOGIFRYVKSALAKMGQRRKND 213
 Db 198 HTKHNPGRGTHMEFRIDLLSPDKNPGLIKWEDSEGFRLKSEAVAOIMGKKNNSS 257
 QY 214 MTEKLSRALRYKYKTLGERVD-RRLVYKFGKNAHQEDK 254
 Db 258 MTEKLSRAMRYKYKREILERVGRRLVYKFGKNAHQRENE 299

RESULT 13

ID 099K12 PRELIMINARY; PRT; 285 AA.
 AC 099K12:
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SIMILAR TO ETS HOMOLOGOUS FACTOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005520; AAH05520.1; -
 DR HSSP: Q00422; IAWC.
 DR InterPro: IPR000418; Ets.
 DR InterPro: IPR002341; HSF_ETS.
 DR InterPro: IPR003118; SAM_PNT.
 DR Pfam: PF00178; SAM_PNT.
 DR Pfam: PF02198; Ets; 1.
 DR PRINTS: PRO0454; ETSDOMAIN.
 DR SMART: SM00413; ETS; 1.
 DR SMART: SM00251; SAM_PNT; 1.
 DR PROSITE: PS50061; ETS_DOMAIN; 3; 1.
 DR SEQUENCE 285 AA; 33225 MW; 91338C527C65955F CRC64;

Query Match 35.5%; Score 514; DB 11; Length 285;
 Best Local Similarity 39.7%; Pred. No. 1.3e-41;
 Matches 112; Conservative 37; Mismatches 64; Indels 69; Gaps 8;

QY 22 SMTDLFSNEEYYPAREHOTACDYSYTSVHPREYWKRRHWEMLOFCCDQYKLDINCISFCN 81
 Db 23 AWTDSYPTCNVSSGF-----FGSOWHEIHPOYWKYQVEMLOHLLDINQDASCIPIFOE 77
 QY 82 FNISGLQCSMTQEEFEVNAAGLCEGYLYFIIONIRTOG-----YSPFNDAEESKA 131
 Db 76 FDISGHEHCSMSLOEFTTRAAGAGQLLYSNLOHLKMGCCSSDLFQSTHNYIVKTEQTEP 137
 QY 121 SPFNDAE-----SKATIKDYADSNCLKTSGI-----KSD-----CHS 154
 Db 123 SIMNTWKEENYLYDPSYGVLDLSDKTCFRAQISMTTSHLPVASEPDKKEQDPAPAC 197
 QY 155 HSRT-SLSOSHMEFVRDLLSPENCILWEDEBOGIFRYVKSALAKMGQRRKND 213
 Db 183 HTKHNPGRGTHMEFRIDLLSPDKNPGLIKWEDSEGFRLKSEAVAOIMGKKNNSS 242

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2002, 21:21:50 ; Search time 88.19 Seconds
(without alignments)
500.212 Million cell updates/sec

Title: US-09-786-043-2
Perfect score: 1409
Sequence: 1 MLDVTHSTPLPNASFCDEL.....DRRLVYRFGNAHGQEDKL 255

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1409	100.0	255	4 Q95175	O95175 homo sapien
2	1409	100.0	265	4 Q96Q13	Q96Q13 mus musculu
3	1406	99.8	255	4 Q9UKW5	Q9UKW5 homo sapien
4	1406	99.8	265	4 Q9UKW6	Q9UKW6 homo sapien
5	1338	95.0	253	11 Q921H5	Q921H5 mus musculu
6	1330	94.4	253	11 Q922K6	Q922K6 mus musculu
7	588.5	41.8	277	4 Q9Y5V5	Q9Y5V5 homo sapien
8	584.3	41.5	277	4 Q9H509	Q9H509 homo sapien
9	578	41.0	300	4 Q9Y5V4	Q9Y5V4 homo sapien
10	574	40.7	300	4 Q9NZC4	Q9NZC4 homo sapien
11	574	40.7	300	4 Q9UKF9	Q9UKF9 homo sapien
12	568	40.3	300	11 Q70273	Q70273 mus musculu
13	514.5	36.5	285	11 Q99K12	Q99K12 mus musculu
14	430.5	30.6	371	11 Q35275	Q35275 mus musculu
15	427.5	30.3	348	4 Q99718	Q99718 homo sapien
16	422	30.0	371	4 P78545	P78545 homo sapien

17	299	21.2	335	4	O95238	O95238 homo sapien
18	297	21.1	325	11	Q9WTP3	Q9WTP3 mus musculu
19	294.5	20.9	79	11	Q922E8	Q922E8 mus musculu
20	276	19.6	538	5	Q93320	Q93320 caenorhabdi
21	262	18.6	463	5	Q19695	Q19695 caenorhabdi
22	251.5	17.8	363	5	O97145	O97145 strongyloce
23	234.5	16.6	456	13	Q9W629	Q9W629 xenopus lae
24	234	16.6	432	13	Q93425	Q93425 coturnix co
25	233	16.5	451	13	Q9PU61	Q9PU61 brachydanio
26	226	16.0	485	13	Q9W700	Q9W700 xenopus lae
27	225.5	16.0	211	11	Q922T6	Q922T6 mus musculu
28	224.5	15.9	490	13	Q9YH24	Q9YH24 brachydanio
29	222.5	15.8	455	13	Q919E8	Q919E8 brachydanio
30	222	15.8	463	11	Q920K8	Q920K8 mus musculu
31	220.5	15.6	455	11	Q91XV5	Q91XV5 rattus norv
32	220	15.6	414	13	Q9PUL6	Q9PUL6 brachydanio
33	216.5	15.4	486	11	Q920K7	Q920K7 mus musculu
34	215.5	15.3	462	11	Q920K9	Q920K9 mus musculu
35	214.5	15.2	351	11	Q91YH8	Q91YH8 mus musculu
36	214	15.2	420	5	O17057	O17057 caenorhabdi
37	214	15.2	521	4	O15725	O15725 homo sapien
38	214	15.2	533	4	Q15724	Q15724 homo sapien
39	214	15.2	581	4	Q15723	Q15723 homo sapien
40	213	15.1	521	11	Q9JHC8	Q9JHC8 mus musculu
41	213	15.1	533	11	Q9JHC7	Q9JHC7 mus musculu
42	213	15.1	581	11	Q9JHD0	Q9JHD0 mus musculu
43	213	15.1	593	11	Q9JHC9	Q9JHC9 mus musculu
44	211	15.0	279	5	Q9GZK0	Q9GZK0 bombyx mori
45	208.5	14.8	336	6	O62804	O62804 ovis aries

ALIGNMENTS

RESULT 1

O95175 PRELIMINARY, PRT; 255 AA.
AC O95175
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE E74-LIKE FACTOR 5.
GN ELFS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99054671; PubMed=9840936;
RA Zhou J., Ng A.Y., Tyms M.J., Jermlin L.S., Seth A.K., Thomas R.S.,
RA Kola I.;
RT "A novel transcription factor, ELF5, belongs to the ELF subfamily of
RT ETS genes and maps to human chromosome 11p13-15, a region subject to
RT LOH and rearrangement in human carcinoma cell lines.";
RL Oncogene 17:2719-2732(1998).
DR EMBL; AF049703; AAC79755.1;
DR HSSP; Q00422; IAWC.
DR InterPro; IPR000418; ETS.
DR InterPro; IPR002341; HSF_ET5.
DR InterPro; IPR003118; SAM_PNT.
DR Pfam; PF00178; Ets; 1.
DR Pfam; PF02198; SAM_PNT; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR SMART; SM00251; SAM_PNT; 1.
DR PROSITE; PS00061; ETS_DOMAIN_3; 1.
SQ SEQUENCE 255 AA; 30121 MW; AE61C5B178ECB555 CRC64;

Query Match 100.0%; Score 1409; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 6.1e-128;
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLDVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPFAFEHOTACDSYWTSVHPHYWTKRHW 60
|||||
DB 1 MLDVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPFAFEHOTACDSYWTSVHPHYWTKRHW 60
61 EWLQFCCDQYKLDTCNCSFNCNLSGLQCSMTQEEFVEAAGLGCGLYLYFILONIRTOGY 120
|||||
DB 61 EWLQFCCDQYKLDTCNCSFNCNLSGLQCSMTQEEFVEAAGLGCGLYLYFILONIRTOGY 120
QY 121 SFFNDAEESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLEWFEVRDRLLSPEENC 180
|||||
DB 121 SFFNDAEESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLEWFEVRDRLLSPEENC 180
QY 181 GILEWEDREOGIFRVVKSALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240
|||||
DB 181 GILEWEDREOGIFRVVKSALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240
QY 241 YKFGKNAHGWOEDKL 255
|||||
DB 241 YKFGKNAHGWOEDKL 255

RESULT 2
Q96QY3 PRELIMINARY; PRT; 265 AA.
ID Q96QY3
AC Q96QY3
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE DJ59419.1 (E74-LIKE FACTOR 5 (ETS DOMAIN TRANSCRIPTION
FACTOR)).
GN ELP5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomas D.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; ALI37224; CAC48256.1;
SQ SEQUENCE 265 AA; 31263 MW; 43821A79A45768FE CRC64;
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Query Match 100.0%; Score 1409; DB 4; Length 265;
Best Local Similarity 100.0%; Pred. No. 6.4e-128;
Matches 255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MLDVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPFAFEHOTACDSYWTSVHPHYWTKRHW 60
|||||
DB 11 MLDVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPFAFEHOTACDSYWTSVHPHYWTKRHW 70
61 EWLQFCCDQYKLDTCNCSFNCNLSGLQCSMTQEEFVEAAGLGCGLYLYFILONIRTOGY 120
|||||
DB 71 EWLQFCCDQYKLDTCNCSFNCNLSGLQCSMTQEEFVEAAGLGCGLYLYFILONIRTOGY 130
QY 121 SFFNDAEESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLEWFEVRDRLLSPEENC 180
|||||
DB 131 SFFNDAEESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLEWFEVRDRLLSPEENC 190
QY 181 GILEWEDREOGIFRVVKSALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240
|||||
DB 191 GILEWEDREOGIFRVVKSALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 250
QY 241 YKFGKNAHGWOEDKL 255
|||||
DB 251 YKFGKNAHGWOEDKL 265

RESULT 3
Q9UKW5 PRELIMINARY; PRT; 255 AA.
ID Q9UKW5
AC Q9UKW5
```

```
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ETS TRANSCRIPTION FACTOR ESE-2B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99436157; PubMed=10506207;
RA Oettgen P., Kas K., Dube A., Gu X., Grall F., Thamrongsak U.,
RA Akbarali Y., Finger E., Boltax J., Endress G., Munger K., Kunsch C.,
RA Libermann T.A.;
RT "Characterization of ESE-2, a novel ESE-1-related Ets transcription
factor that is restricted to glandular epithelium and differentiated
keratinocytes."
RT J. Biol. Chem. 274:29439-29452(1999).
EL EMBL; AF115403; AAD22961.1;
DR HSSP; Q00422; IAWC.
DR InterPro; IPR000418; Ets.
DR InterPro; IPR002341; HSF_ETS.
DR InterPro; IPR003118; SAM_PNT.
DR Pfam; PF00178; Ets; 1.
DR Pfam; PF02198; SAM_PNT; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR SMART; SM00251; SAM_PNT; 1.
DR PROSITE; PSS0061; ETS_DOMAIN_3; 1.
SQ SEQUENCE 255 AA; 30153 MW; 5F71C5B178ECB548 CRC64;
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Query Match 99.8%; Score 1406; DB 4; Length 255;
Best Local Similarity 99.6%; Pred. No. 1.2e-127;
Matches 254; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MLDVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPFAFEHOTACDSYWTSVHPHYWTKRHW 60
|||||
DB 1 MLDVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPFAFEHOTACDSYWTSVHPHYWTKRHW 60
61 EWLQFCCDQYKLDTCNCSFNCNLSGLQCSMTQEEFVEAAGLGCGLYLYFILONIRTOGY 120
|||||
DB 61 EWLQFCCDQYKLDTCNCSFNCNLSGLQCSMTQEEFVEAAGLGCGLYLYFILONIRTOGY 120
QY 121 SFFNDAEESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLEWFEVRDRLLSPEENC 180
|||||
DB 121 SFFNDAEESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLEWFEVRDRLLSPEENC 180
QY 181 GILEWEDREOGIFRVVKSALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240
|||||
DB 181 GILEWEDREOGIFRVVKSALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240
QY 241 YKFGKNAHGWOEDKL 255
|||||
DB 241 YKFGKNAHGWOEDKL 255
```

```
RESULT 4
Q9UKW6 PRELIMINARY; PRT; 265 AA.
ID Q9UKW6
AC Q9UKW6
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ETS TRANSCRIPTION FACTOR ESE-2A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99436157; PubMed=10506207;
RA Oettgen P., Kas K., Dube A., Gu X., Grall F., Thamrongsak U.,
```

RA Akbarali Y., Finger E., Boltax J., Endress G., Munger K., Kunsch C.,
 RA Libermann T.A.;
 RT "Characterization of ESE-2, a novel ESE-1-related Ets transcription
 factor that is restricted to glandular epithelium and differentiated
 keratinocytes.";
 RL J. Biol. Chem. 274:29439-29452(1999).
 DR EMBL; AF115402; AAD22960.1; -;
 DR HSP; Q00422; IAWC.
 DR InterPro; IPR000418; Ets.
 DR InterPro; IPR002341; HSF_ET5.
 DR InterPro; IPR003118; SAM_PNT.
 DR Pfam; PF00178; Ets; 1.
 DR Pfam; PF02198; SAM_PNT; 1.
 DR PRINTS; PR00454; ETSDOMAIN.
 DR SMART; SM00413; ETS; 1.
 DR SMART; SM00251; SAM_PNT; 1.
 DR PROSITE; PS0061; ETS_DOMAIN_3; 1.
 SQ SEQUENCE 265 AA; 31295 MW; B2921A79A45768E3 CRC64;

Query Match 99.8%; Score 1406; DB 4; Length 265;
 Best Local Similarity 99.6%; Pred. No. 1.2e-127;
 Matches 254; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLDSVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPAFEHQTACDSYWTSVHPYWKRVHW 60
 Db 11 MLDSVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPAFEHQTACDSYWTSVHPYWKRVHW 70
 QY 61 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQEEFVEAAGLCGEYLYFILONIRTOGY 120
 Db 71 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQEEFVEAAGLCGEYLYFILONIRTOGY 130
 QY 121 SFFNDAESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLMWFEFVDRDLRLV 180
 Db 131 SFFNDAESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLMWFEFVDRDLRLV 190
 QY 181 GILEWEDREOGIFRVVKSALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240
 Db 191 GILEWEDREOGIFRVVKSALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 250
 QY 241 YKFGKNAHGQEDKL 255
 Db 251 YKFGKNAHGQEDKL 265

RESULT 5
 Q921H5 PRELIMINARY; PRT; 253 AA.
 ID Q921H5
 AC Q921H5
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DE SIMILAR TO E74-LIKE FACTOR 5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC012424; AAH12424.1; -;
 SQ SEQUENCE 253 AA; 29872 MW; 3FC4799F77AFCF48 CRC64;

Query Match 95.0%; Score 1338; DB 11; Length 253;
 Best Local Similarity 94.5%; Pred. No. 4.2e-121;
 Matches 241; Conservative 8; Mismatches 4; Indels 2; Gaps 1;

QY 1 MLDSVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPAFEHQTACDSYWTSVHPYWKRVHW 60
 Db 1 MLDSVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPAFEHQTACDSYWTSVHPYWKRVHW 60

QY 61 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQEEFVEAAGLCGEYLYFILONIRTOGY 120
 Db 61 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQEEFVEAAGLCGEYLYFILONIRTOGY 120
 QY 121 SFFNDAESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLMWFEFVDRDLRLV 180
 Db 121 SFFNDAESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLMWFEFVDRDLRLV 178
 QY 181 GILEWEDREOGIFRVVKSALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240
 Db 179 GILEWEDREOGIFRVVKSALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 238
 QY 241 YKFGKNAHGQEDKL 255
 Db 239 YKFGKNAHGQEDKL 253
 RESULT 6
 Q922K6 PRELIMINARY; PRT; 253 AA.
 ID Q922K6
 AC Q922K6
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE E74-LIKE FACTOR 5.
 GN ELF5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95054671; PubMed=9840936;
 RA Zhou J., Ng A.Y., Tyms M.J., Jermin L.S., Seth A.K., Thomas R.S.,
 RA Kola I.;
 RT "A novel transcription factor, ELF5, belongs to the ELF subfamily of
 ETS genes and maps to human chromosome 11p13-15, a region subject to
 LOH and rearrangement in human carcinoma cell lines.";
 RT Oncogene 17:2719-2732(1998).
 RL EMBL; AF049702; AAC79754.1; -;
 DR HSP; Q00422; IAWC.
 DR MGD; MGI:1335079; Elf5.
 DR InterPro; IPR000418; Ets.
 DR InterPro; IPR002341; HSF_ET5.
 DR InterPro; IPR003118; SAM_PNT.
 DR Pfam; PF00178; Ets; 1.
 DR Pfam; PF02198; SAM_PNT; 1.
 DR PRINTS; PR00454; ETSDOMAIN.
 DR SMART; SM00413; ETS; 1.
 DR SMART; SM00251; SAM_PNT; 1.
 DR PROSITE; PS0061; ETS_DOMAIN_3; 1.
 SQ SEQUENCE 253 AA; 29971 MW; 3FD028DA77AFCF48 CRC64;

Query Match 94.4%; Score 1330; DB 11; Length 253;
 Best Local Similarity 94.1%; Pred. No. 2.5e-120;
 Matches 240; Conservative 8; Mismatches 5; Indels 2; Gaps 1;

QY 1 MLDSVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPAFEHQTACDSYWTSVHPYWKRVHW 60
 Db 1 MLDSVTHSTFLPNASFCDFPLMSWTDLFSNEEYYPAFEHQTACDSYWTSVHPYWKRVHW 60
 QY 61 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQEEFVEAAGLCGEYLYFILONIRTOGY 120
 Db 61 EWLOFCCDOYKLDNTNCISFCNFNISGLQCSMTQEEFVEAAGLCGEYLYFILONIRTOGY 120
 QY 121 SFFNDAESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLMWFEFVDRDLRLV 180
 Db 121 SFFNDAESKATIKDYADSNCLKTSGIKSQDCHSHSRSTSLOSSHLMWFEFVDRDLRLV 178
 QY 181 GILEWEDREOGIFRVVKSALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 240
 Db 179 GILEWEDREOGIFRVVKSALAKMWGQKKNDRMTYEKLSRALRYYYKTGILERVDRRLV 238

QY 241 YKFGKNAHQWEDKL 255
 Db 239 YKFGKNAHQWEDKL 253

RESULT 7
 QY95V5 PRELIMINARY; PRT; 277 AA.
 AC QY95V5;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE TRANSCRIPTION FACTOR ESE-3A.
 GN ESE-3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PROSTATE GLAND;
 RX MEDLINE=20112875; PubMed=10644770;
 RA Kas K., Finger E., Grall F., Gu X., Akbarali Y., Boltax J., Weiss A.,
 RA Oettgen P., Kapeller R., Libermann T.A.;
 RT "ESE-3, a Novel Member of an Epithelium-specific Ets Transcription
 Factor Subfamily, Demonstrates Different Target Gene Specificity from
 ESE-1.";
 RL J. Biol. Chem. 275:2986-2998(2000).
 DR EMBL; AF124438; AAD30990.1;
 DR HSP; Q00422; IAWC.
 DR InterPro; IPR000418; Ets.
 DR InterPro; IPR002341; HSF-ETS.
 DR InterPro; IPR003118; SAM_PNT.
 DR Pfam; PF00178; Ets; 1.
 DR Pfam; PF02198; SAM_PNT; 1.
 DR PRINTS; SM00454; ETSDOMAIN.
 DR SMART; SM00251; SAM_PNT; 1.
 DR SMART; PS0061; ETS_DOMAIN_3; 1.
 DR PROSITE; 277 AA; 32375 MW; 8094FB8547C964A3 CRC64;
 SQ SEQUENCE 277 AA; 32375 MW; 8094FB8547C964A3 CRC64;

Query Match 41.88; Score 588.5; DB 4; Length 277;
 Best Local Similarity 44.68; Pred. No. 9.4e-49;
 Matches 116; Conservative 47; Mismatches 64; Indels 33; Gaps 7;

QY 22 SWTDLFSNEEYYPAFEHQACDSYVTSVHPEYTKRHWELQFCDDQYKLDTCISFCN 81
 Db 23 AWTDSYSTCNVSGF-----FGSQWHEIHPOYWKYQWELQHLDTNQLDANCIPQE 77
 QY 82 FNISGLQCSMTQEEFVEAAGLCEYLYFLQNTQ-----YSPFNDAEESKA 131
 Db 78 FDINGEHLCSMSLOEFTRAAGTAGOLLYSLNQLKWNQCSDDLFSQTHNVIVKTEQEP 137
 QY 132 TKID-YADSNCLKTSGI-----KSOD---CHSHRTSLQSHLWFEVRDILLS 175
 Db 138 SIMTWKDNLYDTNTGTVAESPDMMKKEQPPAKCHT-KKHNPGRGTHLWFEVRDILLN 196
 QY 176 PEENCGILEWEDRQGIFFRVVKSEALAKMWGORKKNDRTYKLSRALRYYYKGTILERV 235
 Db 197 PDKNPGLIKWEDRSEGVRFLKSEAVQLWGLKNNSSMTYKLSRAMRYYYKREILERV 256
 QY 236 D-RLVYKFGKNAHQWEDK 254
 Db 257 DGRRLVYKFGKNARGWRENE 276

RESULT 8
 QY9H509 PRELIMINARY; PRT; 277 AA.
 AC QY9H509;
 DT 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE DJ875K15.1.1 (ETS HOMOLOGOUS FACTOR (ETS-DOMAIN TRANSCRIPTION FACTOR
 DE ESE-3A, ISOFORM 1)).
 GN EHF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hall R.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL157952; CAC12700.1;
 DR HSP; Q00422; IAWC.
 DR InterPro; IPR000418; Ets.
 DR InterPro; IPR002341; HSF-ETS.
 DR InterPro; IPR003118; SAM_PNT.
 DR Pfam; PF00178; Ets; 1.
 DR Pfam; PF02198; SAM_PNT; 1.
 DR PRINTS; SM00454; ETSDOMAIN.
 DR SMART; SM00251; SAM_PNT; 1.
 DR SMART; PS0061; ETS_DOMAIN_3; 1.
 DR PROSITE; 277 AA; 32345 MW; 3BF620E8F1164811 CRC64;
 SQ SEQUENCE 277 AA; 32345 MW; 3BF620E8F1164811 CRC64;

Query Match 41.58; Score 584.5; DB 4; Length 277;
 Best Local Similarity 44.28; Pred. No. 2.3e-48;
 Matches 115; Conservative 47; Mismatches 65; Indels 33; Gaps 7;

QY 22 SWTDLFSNEEYYPAFEHQACDSYVTSVHPEYTKRHWELQFCDDQYKLDTCISFCN 81
 Db 23 AWTDSYSTCNVSGF-----FGSQWHEIHPOYWKYQWELQHLDTNQLDANCIPQE 77
 QY 82 FNISGLQCSMTQEEFVEAAGLCEYLYFLQNTQ-----YSPFNDAEESKA 131
 Db 78 FDINGEHLCSMSLOEFTRAAGTAGOLLYSLNQLKWNQCSDDLFSQTHNVIVKTEQEP 137
 QY 132 TKID-YADSNCLKTSGI-----KSOD---CHSHRTSLQSHLWFEVRDILLS 175
 Db 138 SIMTWKDNLYDTNTGTVAESPDMMKKEQPPAKCHT-KKHNPGRGTHLWFEVRDILLN 196
 QY 176 PEENCGILEWEDRQGIFFRVVKSEALAKMWGORKKNDRTYKLSRALRYYYKGTILERV 235
 Db 197 PDKNPGLIKWEDRSEGVRFLKSEAVQLWGLKNNSSMTYKLSRAMRYYYKREILERV 256
 QY 236 D-RLVYKFGKNAHQWEDK 254
 Db 257 DGRRLVYKFGKNARGWRENE 276

RESULT 9
 QY95V4 PRELIMINARY; PRT; 300 AA.
 ID QY95V4;
 AC QY95V4;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE TRANSCRIPTION FACTOR ESE-3B.
 GN ESE-3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PROSTATE GLAND;
 RX MEDLINE=20112875; PubMed=10644770;
 RA Kas K., Finger E., Grall F., Gu X., Akbarali Y., Boltax J., Weiss A.,
 RA Oettgen P., Kapeller R., Libermann T.A.;
 RT "ESE-3, a Novel Member of an Epithelium-specific Ets Transcription
 Factor Subfamily, Demonstrates Different Target Gene Specificity from


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DR InterPro: IPR003118; SAM_PNT.
DR Pfam: PF00178; Ets; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR SMART; SM00251; SAM_PNT; 1.
DR PROSITE; PS50061; ETS_DOMAIN_3; 1.
SQ SEQUENCE 300 AA; 34893 MW; 51CB68B6195E4E06 CRC64;

Query Match 40.7%; Score 574; DB 4; Length 300;
Best Local Similarity 41.3%; Pred. No. 2.6e-47;
Matches 117; Conservative 47; Mismatches 63; Indels 56; Gaps 8;

QY 22 SWTDLFSNEEYPAFEHQTCADSYVTHPEYTKRHWLWVWELQCCDQYKLDTCNISCN 81
Db 23 AWTDSYPTCNVSSGF-----FGQWHEIHPQYTKYQVWELQHLDTNQLDASCIPQE 77
QY 82 FNISGLQCSMTQEEFVEAAGLCGEYLYFILONRTQGY-----YSFENDAEESKA 131
Db 78 FDINGEHLCSMSLQEFTRAAGTAGQLLYSLNQLHLKWNQCSSDLFQSTHNVIVKTEQTEP 137
QY 132 TIKD-YADSNCL-----KTSGI-----KSQD-----C 152
Db 138 SIMTWKDNLYDNTYGVSTVDLLDSTFCRAQISMTTSHLPVAESPDMMKKEODPPAEC 197
QY 153 HSRSTLSQSHLWFEVRDILLSPENCIGLEWEDREGIFRVVVKSEALAKMMGORKKND 212
Db 198 HT-KKHNRGTHLWFEVRDILLSPENCIGLEWEDREGIFRVVVKSEALAKMMGORKKNS 256
QY 213 RMYEKLRSALRYKYKTGILERVD-RLVYKFGKNAHQWQEDK 254
Db 257 SMTYEKLRSAMRYKYKREILERVDRGLVYKFGKNARGWRENE 299

RESULT 12
O70273 PRELIMINARY; PRT; 300 AA.
AC O70273
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE EHF.
GN EHF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PITUITARY;
RX MEDLINE=98262938; PubMed=9600089;
RA Bocher M.A., Kleinbaum L.A., Sun L.Y., Burton F.H.;
RT "Molecular cloning and expression of Ehf, a new member of the ets
transcription factor/oncoprotein gene family.";
RL Biochem. Biophys. Res. Commun. 246:176-181(1998).
DR EMBL; AF035527; AAC40119.1; .
DR HSSP; Q00422; IAWC.
DR MGD; MGI:1270840; Ehf.
DR InterPro; IPR000418; Ets.
DR InterPro; IPR002341; HSF_ETs.
DR InterPro; IPR003118; SAM_PNT.
DR Pfam; PF00178; Ets; 1.
DR Pfam; PF02198; SAM_PNT; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00251; SAM_PNT; 1.
DR SMART; SM00413; ETS; 1.
DR PROSITE; PS50061; ETS_DOMAIN_3; 1.
SQ SEQUENCE 300 AA; 34903 MW; 91D9477EFB874747 CRC64;

Query Match 40.3%; Score 568; DB 11; Length 300;
Best Local Similarity 42.6%; Pred. No. 9.9e-47;

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Matches 120; Conservative 39; Mismatches 69; Indels 54; Gaps 7;

QY 22 SWTDLFSNEEYPAFEHQTCADSYVTHPEYTKRHWLWVWELQCCDQYKLDTCNISCN 81
Db 23 AWTDSYPTCNVSSGF-----FGQWHEIHPQYTKYQVWELQHLDTNQLDASCIPQE 77
QY 82 FNISGLQCSMTQEEFVEAAGLCGEYLYFILONRTQGY----- 120
Db 78 FDINGEHLCSMSLQEFTRAAGTAGQLLYSLNQLHLKWNQCSSDLFQSAHNVIVKTEQTD 137
QY 121 SFNDAAE-----SKATIKDYADSNCLKTSGI-----KSQD-----CHS 154
Db 138 SIMTWKDNLYDNTYGVSTVDLLDSTFCRAQISMTTSHLPVAESPDMMKKEODHPVKS 197
QY 155 HSRT-SLQSHLWFEVRDILLSPENCIGLEWEDREGIFRVVVKSEALAKMMGORKKND 213
Db 198 HTKHNPRGTHLWFEVRDILLSPENCIGLEWEDREGIFRVVVKSEALAKMMGORKKNS 257
QY 214 MYEKLRSALRYKYKTGILERVD-RLVYKFGKNAHQWQEDK 254
Db 258 MTYEKLRSAMRYKYKREILERVDRGLVYKFGKNARGWRENE 299

RESULT 13
Q99K12 PRELIMINARY; PRT; 285 AA.
AC Q99K12
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SIMILAR TO ETS HOMOLOGOUS FACTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005520; AAH05520.1; .
DR HSSP; Q00422; IAWC.
DR InterPro; IPR000418; Ets.
DR InterPro; IPR002341; HSF_ETs.
DR InterPro; IPR003118; SAM_PNT.
DR Pfam; PF00178; Ets; 1.
DR Pfam; PF02198; SAM_PNT; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR SMART; SM00251; SAM_PNT; 1.
DR PROSITE; PS50061; ETS_DOMAIN_3; 1.
SQ SEQUENCE 285 AA; 33225 MW; 91398C527C65955F CRC64;

Query Match 36.5%; Score 514.5; DB 11; Length 285;
Best Local Similarity 39.7%; Pred. No. 1.3e-41;
Matches 112; Conservative 37; Mismatches 64; Indels 69; Gaps 8;

QY 22 SWTDLFSNEEYPAFEHQTCADSYVTHPEYTKRHWLWVWELQCCDQYKLDTCNISCN 81
Db 23 AWTDSYPTCNVSSGF-----FGQWHEIHPQYTKYQVWELQHLDTNQLDASCIPF-- 75
QY 82 FNISGLQCSMTQEEFVEAAGLCGEYLYFILONRTQGY----- 120
Db 76 -----QEFTRAAGTAGQLLYSLNQLHLKWNQCSSDLFQSAHNVIVKTEQTD 122
QY 121 SFNDAAE-----SKATIKDYADSNCLKTSGI-----KSQD-----CHS 154
Db 123 SIMTWKDNLYDNTYGVSTVDLLDSTFCRAQISMTTSHLPVAESPDMMKKEODHPVKS 182
QY 155 HSRT-SLQSHLWFEVRDILLSPENCIGLEWEDREGIFRVVVKSEALAKMMGORKKND 213
Db 183 HTKHNPRGTHLWFEVRDILLSPENCIGLEWEDREGIFRVVVKSEALAKMMGORKKNS 242

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Db 358 SSGWKEEV 366

Search completed: August 13, 2002, 21:31:15
Job time: 565 sec

